

## WEST Search History





DATE: Wednesday, June 22, 2005

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,EPAB,JPAB; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L22	(acyl adj transferase) same gene	169
<input type="checkbox"/>	L21	L20 and (transacylase or acyltransferase or transferase)	13
<input type="checkbox"/>	L20	1999	60
<input type="checkbox"/>	L19	L18 same (transform\$6 or transgen\$4 or exogenous)	398
<input type="checkbox"/>	L18	(triacylglycerol or triglyceride) same (produc\$6 or make or \$4synthesi\$5)	12976
<input type="checkbox"/>	L17	cerevisiae same (triacylglycerol or triglyceride) same (produc\$6 or make or \$4synthesi\$5)	18
<input type="checkbox"/>	L16	cerevisiae same (triacylglycerol or triglyceride) same (transform\$6 or transgen\$4 or exogenous)	5
<input type="checkbox"/>	L15	1999	6
<input type="checkbox"/>	L14	L13 same(express\$4 or transcri\$5 or \$6produc\$4)	138
<input type="checkbox"/>	L13	L12 same (DGAT or ACAT or diacyl\$10)	182
<input type="checkbox"/>	L12	(transacylase or acyltransferase or transferase) same (triacylglycerol or triglyceride)	636
<input type="checkbox"/>	L11	L10 and triacylglycerol	576
<input type="checkbox"/>	L10	(transacylase or acyltransferase or transferase)	41496
<input type="checkbox"/>	L9	1999	7
<input type="checkbox"/>	L8	1999	4
<input type="checkbox"/>	L7	L6 same (express\$4 or transcri\$5 or \$6produc\$4)	74
<input type="checkbox"/>	L6	L4 same (DGAT or ACAT or diacyl\$10)	107
<input type="checkbox"/>	L5	L4 same (DGAT or ACAT)	25
<input type="checkbox"/>	L4	(transacylase or acyltransferase or transferase) same triacylglycerol	188

END OF SEARCH HISTORY

STN SEARCH SUMMARY  
09/937779

=> d his

FILE 'CAPLUS' ENTERED AT 14:36:18 ON 22 JUN 2005  
L2 58760 S (TRANSACYLASE OR ACYLTRANSFERASE OR TRANSFERASE)  
L3 11564 S TRIACYLGLYCEROL  
L4 770 S L2 AND L3  
L5 508 S L4 AND PD<1999  
L6 1451 S L5 AND DAGAT OR ACAT  
L7 39 S L5 AND (DAGAT OR ACAT)  
L8 574 S L4 AND (DAGAT OR ACAT OR DIACYLGLYCEROL OR CHOLESTEROL)  
L9 24 S L8 AND CEREVISIAE

# SEQUENCE SEARCH SUMMARY

## 09/937779

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 13:58:51 ; Search time 8752 Seconds  
(without alignments)  
10995.436 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1986	100.0	1986	6	BD271616	BD271616 Novel cla
2	1986	100.0	1986	6	BD271625	BD271625 Novel cla
3	1986	100.0	1986	6	BD271626	BD271626 Novel cla

	4	1986	100.0	1986	6	AX037577	WU 2000	AX037577	Sequence
	5	1986	100.0	1986	6	AX037595	//	AX037595	Sequence
	6	1986	100.0	1986	6	AX037597	//	AX037597	Sequence
	7	1986	100.0	1986	6	AX090382	WU 2001	AX090382	Sequence
	8	1986	100.0	2575	8	SCYNR008W	4/1996 S/B project	Z71623	S.cerevisia
	9	1986	100.0	23901	8	SCN201952	1994 Verhasselt	X77395	S.cerevisia
c	10	835.6	42.1	110000	8	CR380955_05	2004	Continuation (6 of	
c	11	715.2	36.0	110000	8	CR382126_06		Continuation (7 of	
c	12	676.2	34.0	110000	8	AE016819_00		AE016819 Erethrothec	
c	13	676.2	34.0	110000	8	AE016819_01		Continuation (2 of	
	14	555.6	28.0	110000	8	CR382136_07		Continuation (8 of	
	15	555.6	28.0	110000	8	CR382136_08		Continuation (9 of	
	16	537	27.0	2106	6	AR546016		AR546016 Sequence	
c	17	439.8	22.1	110000	8	CR382131_19		Continuation (20 o	
	18	273.4	13.8	103568	8	CNS07EGJ		AL590462	DNA centr
c	19	273.4	13.8	322194	8	CNS09S4S		BX088700	DNA centr
	20	202	10.2	2312	6	BD271617		BD271617	Novel cla
	21	202	10.2	2312	6	BD271627		BD271627	Novel cla
	22	202	10.2	2312	6	AX037579		AX037579	Sequence
	23	202	10.2	2312	6	AX037599		AX037599	Sequence
	24	202	10.2	42391	8	SPBC776		AL035263	S.pombe c
	25	137.2	6.9	2441	8	BT013705		BT013705	Lycopersi
	26	129.2	6.5	2828	8	AY210981		AY210981	Medicago
	27	127.2	6.4	2433	6	AX794708		AX794708	Sequence
	28	127.2	6.4	2495	8	AK100079		AK100079	Oryza sat
	29	125.6	6.3	3203	8	AK099811		AK099811	Oryza sat
	30	124	6.2	2398	6	AX794712		AX794712	Sequence
	31	117.6	5.9	2565	6	AX794706		AX794706	Sequence
	32	117.4	5.9	2013	6	AX090380		AX090380	Sequence
	33	117.4	5.9	2016	6	AX412864		AX412864	Sequence
	34	117.4	5.9	2402	8	AY052715		AY052715	Arabidops
	35	117.4	5.9	2425	6	AX925713		AX925713	Sequence
	36	117.4	5.9	2427	6	BD271619		BD271619	Novel cla
	37	117.4	5.9	2427	6	AX037581		AX037581	Sequence
	38	117.4	5.9	2431	8	AY160110		AY160110	Arabidops
	39	116.6	5.9	2030	6	AX794714		AX794714	Sequence
	40	115.4	5.8	2700	6	AX794710		AX794710	Sequence
	41	114.4	5.8	2479	6	AX794704		AX794704	Sequence
	42	105.4	5.3	4093	6	AX794722		AX794722	Sequence
	43	101.6	5.1	1945	8	PPA493274		AJ493274	Physcomit
c	44	82.4	4.1	87724	8	AY448010S4		AY448013	Ipomoea t
	45	67.6	3.4	2914	8	PPA493276		AJ493276	Physcomit

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 11:44:51 ; Search time 1103 Seconds  
(without alignments)  
10658.755 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	1986	100.0	1986	3	AAC64431	App1	Aac64431 Saccharom
2	1986	100.0	1986	3	AAC64440	"	Aac64440 Saccharom
3	1986	100.0	1986	5	AAS01342	WO '01	Aas01342 Yeast LCA
4	1986	100.0	1986	12	ADF47816	bp1 2002	Adf47816 Yeast acy

	5	1958.8	98.6	1986	3	AAC64441	App1	Aac64441	Saccharom
	6	1694.4	85.3	1701	12	ADF47817		Adf47817	Yeast mem
	7	309.2	15.6	1872	12	ADF47831		Adf47831	Schizosac
	8	254	12.8	2223	12	ADF47830		Adf47830	Aspergill
c	9	238	12.0	7299	13	ADR84383	2003	Adr84383	Aspergill
	10	217.6	11.0	2047	12	ADF47829	App1	Adf47829	Aspergill
	11	202	10.2	2312	3	AAC64442		Aac64442	Schizosac
	12	202	10.2	2312	3	AAC64432		Aac64432	Schizosac
	13	133.8	6.7	2004	12	ADF47835		Adf47835	Crepis pa
	14	127.2	6.4	2433	9	AAL62907	2001	Aal62907	Rice cDNA
	15	126.6	6.4	2016	12	ADF47833	2002	Adf47833	Crepis pa
	16	124	6.2	1998	8	ABZ76360		Abz76360	A. thalia
	17	124	6.2	1998	12	ADF47827		Adf47827	Arabidops
	18	124	6.2	2398	9	AAL62909		Aal62909	Sunflower
	19	117.6	5.9	2565	9	AAL62906		Aal62906	Corn cDNA
	20	117.4	5.9	1803	12	ADF47821		Adf47821	Arabidops
	21	117.4	5.9	2013	5	AAS01341		Aas01341	Arabidops
	22	117.4	5.9	2016	6	ADG88186		Adg88186	A. thalia
	23	117.4	5.9	2016	12	ADF47819		Adf47819	Arabidops
	24	117.4	5.9	2425	10	ADG25155		Adg25155	P. patens
	25	117.4	5.9	2427	3	AAC64434		Aac64434	Arabidops
	26	117	5.9	553	8	ABZ54921		Abz54921	Aspergill
	27	116.6	5.9	2030	9	AAL62910		Aal62910	Wheat cDN
	28	115.4	5.8	2700	9	AAL62908		Aal62908	Soybean c
	29	114.4	5.8	2479	9	AAL62905		Aal62905	Guayule c
	30	105.4	5.3	4093	9	AAL62913		Aal62913	Soybean c
	31	103.4	5.2	578	13	ADR61378		Adr61378	Cotton cD
	32	63.8	3.2	419	5	AAS01089		Aas01089	Soybean s
	33	63.4	3.2	3107	5	AAS01085		Aas01085	Arabidops
	34	63.4	3.2	3685	3	AAC64433		Aac64433	Arabidops
	35	63.4	3.2	3685	3	AAC64443		Aac64443	Arabidops
	36	59.2	3.0	616	3	AAC64436		Aac64436	Neurospor
	37	58.6	3.0	254	5	AAS01104		Aas01104	Corn ster
	38	58.4	2.9	1510	9	AAL62904		Aal62904	Guar cDNA
c	39	54.8	2.8	1680	5	AAS01086		Aas01086	Arabidops
c	40	51	2.6	2000	8	ADA71938		Ada71938	Rice gene
	41	49.4	2.5	1641	5	AAS01082		Aas01082	Arabidops
	42	49.4	2.5	1902	12	ADF47823		Adf47823	Arabidops
	43	45.6	2.3	2000	8	ADA71938		Ada71938	Rice gene
c	44	44.2	2.2	4590	5	AAH24065		Aah24065	Yeast AOD
	45	44	2.2	655	13	ADR63567		Adr63567	Cotton cD

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 15:50:07 ; Search time 355 Seconds  
(without alignments)  
9153.931 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :      Issued_Patents_NA:*
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2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query					Description	
No.	Score	Match	Length	DB	ID			
	1	537	27.0	2106	4	US-09-248-796A-1147	FD=2/99	Sequence 1147, Ap
c	2	55	2.8	7218	1	US-08-232-463-14	X	Sequence 14, Appl
	3	47.4	2.4	1141	4	US-09-806-708B-22	X	Sequence 22, Appl
c	4	42.2	2.1	1141	4	US-09-806-708B-22	X	Sequence 22, Appl
	5	38.6	1.9	1431	4	US-09-248-796A-9904	FD=2/99	Sequence 9904, Ap
c	6	38.6	1.9	24333	4	US-09-639-207-9	X	Sequence 9, Appli
	7	38	1.9	601	4	US-09-949-016-149237	X	Sequence 149237,
c	8	38	1.9	187169	4	US-09-949-016-12776	X	Sequence 12776, A
c	9	38	1.9	191569	4	US-09-949-016-15940	X	Sequence 15940, A
	10	37.4	1.9	552	4	US-09-248-796A-10377	2/99	Sequence 10377, A
	11	37.2	1.9	615	4	US-09-134-000C-1430	1998	Sequence 1430, Ap

6747137  
Patent 102e  
bactenol  
102109

	12	37.2	1.9	1401	4	US-09-248-796A-4906	2/99	Sequence 4906, Ap
	13	37	1.9	31391	4	US-09-949-016-14319	X	Sequence 14319, A
	14	36.8	1.9	8905	4	US-09-949-016-11761	X	Sequence 11761, A
	15	36.8	1.9	8907	4	US-09-949-016-16261	X	Sequence 16261, A
c	16	36.8	1.9	20961	4	US-09-949-016-12902		Sequence 12902, A
c	17	36.8	1.9	640681	4	US-09-790-988-1		Sequence 1, Appli
	18	36.8	1.9	767677	4	US-09-949-016-12147		Sequence 12147, A
	19	36.8	1.9	767677	4	US-09-949-016-17361		Sequence 17361, A
c	20	36.6	1.8	612	3	US-09-328-111-138		Sequence 138, App
	21	36.6	1.8	640681	4	US-09-790-988-1		Sequence 1, Appli
c	22	36.4	1.8	658	3	US-08-998-416-595		Sequence 595, App
	23	36.4	1.8	1251	4	US-09-248-796A-7874		Sequence 7874, Ap
	24	36.4	1.8	2121	4	US-09-134-000C-2129		Sequence 2129, Ap
c	25	36.2	1.8	50950	4	US-09-949-016-16659		Sequence 16659, A
c	26	36	1.8	396	4	US-09-513-999C-19417		Sequence 19417, A
	27	36	1.8	601	4	US-09-949-016-127475		Sequence 127475,
	28	36	1.8	601	4	US-09-949-016-127476		Sequence 127476,
c	29	36	1.8	1038	4	US-09-248-796A-4292		Sequence 4292, Ap
c	30	36	1.8	129327	4	US-09-949-016-12257		Sequence 12257, A
c	31	36	1.8	129327	4	US-09-949-016-15368		Sequence 15368, A
	32	35.8	1.8	360	4	US-09-248-796A-7842		Sequence 7842, Ap
	33	35.8	1.8	2709	4	US-09-614-221A-250		Sequence 250, App
	34	35.8	1.8	3030	4	US-09-328-352-4115		Sequence 4115, Ap
c	35	35.8	1.8	24415	4	US-09-949-016-15855		Sequence 15855, A
	36	35.8	1.8	145812	4	US-09-949-016-15698		Sequence 15698, A
c	37	35.8	1.8	580073	4	US-08-545-528D-1		Sequence 1, Appli
	38	35.6	1.8	695	3	US-08-936-165A-171		Sequence 171, App
c	39	35.6	1.8	832	4	US-09-621-976-2813		Sequence 2813, Ap
c	40	35.6	1.8	1790	4	US-09-016-434-1393		Sequence 1393, Ap
c	41	35.6	1.8	1790	4	US-09-919-497-22		Sequence 22, Appl
c	42	35.6	1.8	14462	4	US-09-843-250-9		Sequence 9, Appli
c	43	35.6	1.8	187595	4	US-09-949-016-15546		Sequence 15546, A
	44	35.6	1.8	1830121	4	US-09-557-884-1		Sequence 1, Appli
	45	35.6	1.8	1830121	4	US-09-643-990A-1		Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 15:32:31 ; Search time 1201 Seconds  
(without alignments)  
10066.732 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8								
Result	Query				Description			
No.	Score	Match	Length	DB	ID			
c	1	436.6	22.0	2326	19	US-10-883-760-45	X	Sequence 45, Appl
	2	128.6	6.5	2395	18	US-10-437-963-38278	X	Sequence 38278, A
	3	127.2	6.4	2433	17	US-10-321-802-21	X	Sequence 21, Appl
	4	124	6.2	1998	16	US-10-217-939-5	X	Sequence 5, Appli
	5	124	6.2	2398	17	US-10-321-802-25	X	Sequence 25, Appl
c	6	117.8	5.9	2700	18	US-10-425-115-55049	X	Sequence 55049, A
	7	117.6	5.9	1388	18	US-10-425-115-55048	X	Sequence 55048, A
	8	117.6	5.9	2565	17	US-10-321-802-19	X	Sequence 19, Appl
	9	116.6	5.9	2030	17	US-10-321-802-27	X	Sequence 27, Appl
	10	115.4	5.8	2700	17	US-10-321-802-23	X	Sequence 23, Appl
	11	114.4	5.8	2479	17	US-10-321-802-17	X	Sequence 17, Appl
	12	105.4	5.3	4093	17	US-10-321-802-35	X	Sequence 35, Appl
	13	103.4	5.2	578	18	US-10-767-795-2159	X	Sequence 2159, Ap
	14	101.8	5.1	2838	17	US-10-424-599-125713	X	Sequence 125713,
	15	66.8	3.4	735	18	US-10-437-963-38267		Sequence 38267, A
	16	58.4	2.9	1510	17	US-10-321-802-15		Sequence 15, Appl
	17	56.2	2.8	1141	17	US-10-424-599-124418		Sequence 124418,
c	18	55.4	2.8	1218	17	US-10-425-114-18228		Sequence 18228, A
	19	55.4	2.8	1239	18	US-10-425-115-71787		Sequence 71787, A
	20	53.2	2.7	887	18	US-10-767-701-9911		Sequence 9911, Ap
	21	49	2.5	693	18	US-10-425-115-55043		Sequence 55043, A
	22	44	2.2	655	18	US-10-767-795-4348		Sequence 4348, Ap
	23	42	2.1	924	18	US-10-425-115-137717		Sequence 137717,
	24	42	2.1	1383	18	US-10-425-115-93909		Sequence 93909, A
	25	41.8	2.1	3673778	16	US-10-312-841-1		Sequence 1, Appli
c	26	41.6	2.1	1659	9	US-09-938-842A-4435		Sequence 4435, Ap
c	27	41.6	2.1	1659	11	US-09-938-842A-4435		Sequence 4435, Ap
	28	41.6	2.1	2790	9	US-09-938-842A-698		Sequence 698, App
	29	41.6	2.1	2790	11	US-09-938-842A-698		Sequence 698, App
c	30	41.4	2.1	468	18	US-10-674-124A-1427		Sequence 1427, Ap
	31	41.4	2.1	599	17	US-10-338-110-117		Sequence 117, App
	32	41.2	2.1	6271	15	US-10-172-086-36		Sequence 36, Appl
	33	41.2	2.1	6271	15	US-10-311-455-1310		Sequence 1310, Ap
	34	41.2	2.1	6271	17	US-10-221-714A-178		Sequence 178, App
	35	41.2	2.1	6271	18	US-10-311-507-62		Sequence 62, Appl
	36	41.2	2.1	6271	18	US-10-480-846-36		Sequence 36, Appl
	37	41	2.1	848	18	US-10-425-115-93907		Sequence 93907, A
	38	41	2.1	5314	15	US-10-311-455-133		Sequence 133, App
	39	41	2.1	5314	16	US-10-240-452-9		Sequence 9, Appli
	40	40.6	2.0	539	10	US-09-814-353-17862		Sequence 17862, A
	41	40.6	2.0	6327	14	US-10-239-676-152		Sequence 152, App
	42	40.6	2.0	6327	15	US-10-240-453-168		Sequence 168, App
	43	40.4	2.0	540	17	US-10-424-599-5143		Sequence 5143, Ap
	44	40	2.0	5879	15	US-10-311-455-242		Sequence 242, App
	45	40	2.0	7201	15	US-10-311-455-310		Sequence 310, App

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 15:27:01 ; Search time 6684 Seconds  
(without alignments)  
11309.940 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			ID	Description
	Score	Match	Length	DB			
1	439	22.1	832	9	CNS060AQ	2000	AL407832 T7 end of
c 2	427.8	21.5	948	9	CNS06Y94	X	AL420734 T3 end of
3	354.6	17.9	609	8	BZ297416	X	BZ297416 CG3420.f1
c 4	324.8	16.4	400	8	AZ924376	X	AZ924376 4906.ic28
5	291.6	14.7	978	9	CNS06TH7	X	AL414545 T7 end of
c 6	249.8	12.6	882	9	CNS07EA9	X	AL441511 T7 end of
c 7	241.2	12.1	474	8	AZ928292	X	AZ928292 479.dif06
c 8	235.4	11.9	509	8	BZ302540	X	BZ302540 KD1890.q1

	9	208.2	10.5	783	7	CO026714 X	CO026714	EST805098
	10	199.6	10.1	512	8	BZ301369 X	BZ301369	KD1229.q1
c	11	194.6	9.8	849	9	CNS06V5M X	AL416720	T7 end of
	12	165.4	8.3	899	7	CO003381 X	CO003381	EST791716
	13	151.2	7.6	970	7	CO032392 X	CO032392	EST810776
c	14	134.2	6.8	550	7	CF884811 ✓	CF884811	tric042xm
	15	129.8	6.5	596	7	CN846346 X	CN846346	PG07016B0
	16	122.6	6.2	605	2	BE450991	BE450991	EST401878
	17	122.2	6.2	719	5	BQ865802	BQ865802	QGC5021.y
	18	119.8	6.0	821	4	BM780050	BM780050	EST590626
	19	118.2	6.0	854	4	BG645669	BG645669	EST507288
	20	117.4	5.9	867	7	CF821111	CF821111	EST698493
	21	116.6	5.9	1490	6	CA731511	CA731511	wiplc.pk0
	22	115.2	5.8	834	7	CF820302	CF820302	EST697684
	23	113.2	5.7	844	6	CB631429	CB631429	OSIEb08P
	24	112.8	5.7	634	5	BQ870476	BQ870476	QGD9C14.y
	25	108.8	5.5	586	1	AV940595	AV940595	AV940595
	26	108.8	5.5	610	4	BJ472152	BJ472152	BJ472152
	27	108.8	5.5	628	4	BJ478864	BJ478864	BJ478864
	28	108.8	5.5	674	4	BJ480170	BJ480170	BJ480170
	29	107.2	5.4	602	6	CA210413	CA210413	SCEPSB112
	30	107.2	5.4	724	5	BQ803421	BQ803421	WHE2837_D
	31	106.2	5.3	569	6	CA018479	CA018479	HV08L24r
	32	104.2	5.2	566	4	BJ470786	BJ470786	BJ470786
	33	102.6	5.2	680	7	CN846719	CN846719	PG07019E0
	34	98.2	4.9	902	7	CF704247	CF704247	CCAC369TR
	35	95	4.8	575	1	AV938810	AV938810	AV938810
	36	94.6	4.8	568	6	CA184037	CA184037	SCQSST311
	37	89	4.5	578	4	BM062412	BM062412	KS01042D1
	38	87.6	4.4	448	6	CA018796	CA018796	HV09K23r
	39	85.8	4.3	631	2	BF053150	BF053150	EST438380
	40	85.8	4.3	869	7	CF685137	CF685137	CCAGP17TR
	41	85.6	4.3	626	2	AW587308	AW587308	EST318931
	42	85.6	4.3	1005	6	CD458189	CD458189	Fg08_10b0
	43	84.8	4.3	477	4	BG313245	BG313245	WHE2051_F
c	44	83.6	4.2	885	7	CF820303	CF820303	EST697685
c	45	83.4	4.2	943	7	CF821110	CF821110	EST698492

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 18:33:57 ; Search time 8752 Seconds  
(without alignments)  
10995.436 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1986	100.0 1986	6	BD271616	BD271616 Novel cla
2	1986	100.0 1986	6	BD271625	BD271625 Novel cla
3	1986	100.0 1986	6	BD271626	BD271626 Novel cla

	4	1986	100.0	1986	6	AX037577	AX037577 Sequence
	5	1986	100.0	1986	6	AX037595	AX037595 Sequence
	6	1986	100.0	1986	6	AX037597	AX037597 Sequence
	7	1986	100.0	1986	6	AX090382	AX090382 Sequence
	8	1986	100.0	2575	8	SCYNR008W	Z71623 S.cerevisia
	9	1986	100.0	23901	8	SCN201952	X77395 S.cerevisia
c	10	26	1.3	135321	2	AC142021X	AC142021 Rattus no
c	11	26	1.3	232722	2	AC112283X	AC112283 Rattus no
c	12	23	1.2	203613	2	AC118575X	AC118575 Lemur cat
c	13	22	1.1	173251	9	AL356280X	AL356280 Human DNA
	14	22	1.1	283341	2	AC128766X	AC128766 Rattus no
c	15	21	1.1	1822	8	D88383	D88383 Hordeum vulgare
	16	21	1.1	1974	3	AF326965	AF326965 Trypanosoma
	17	21	1.1	33744	9	AC027326	AC027326 Homo sapi
	18	21	1.1	78303	9	AC008910	AC008910 Homo sapi
	19	21	1.1	129575	9	AL160159	AL160159 Human DNA
	20	21	1.1	162349	9	AC006226	AC006226 Homo sapi
c	21	21	1.1	165518	3	AC091226	AC091226 Drosophil
	22	21	1.1	167345	5	BX004771	BX004771 Zebrafish
c	23	21	1.1	167638	3	AC069405	AC069405 Drosophil
	24	21	1.1	188048	10	AL669974	AL669974 Mouse DNA
	25	21	1.1	193074	2	AC017576	AC017576 Drosophil
	26	21	1.1	199531	9	AC094104	AC094104 Homo sapi
	27	21	1.1	200028	9	AC092680	AC092680 Homo sapi
	28	21	1.1	200229	10	AC099572	AC099572 Mus muscu
c	29	21	1.1	236957	2	AC118153	AC118153 Rattus no
	30	21	1.1	260198	2	BX469922	BX469922 Danio rer
c	31	21	1.1	282116	3	AE003537	AE003537 Drosophil
c	32	20	1.0	181	9	AY728770	AY728770 Macaca mu
c	33	20	1.0	450	6	CQ050097	CQ050097 Sequence
c	34	20	1.0	450	6	CQ065138	CQ065138 Sequence
c	35	20	1.0	450	6	CQ092094	CQ092094 Sequence
c	36	20	1.0	450	6	CQ130908	CQ130908 Sequence
c	37	20	1.0	450	6	CQ169518	CQ169518 Sequence
c	38	20	1.0	450	6	CQ198654	CQ198654 Sequence
c	39	20	1.0	450	6	CQ214119	CQ214119 Sequence
c	40	20	1.0	450	6	CQ252704	CQ252704 Sequence
c	41	20	1.0	450	6	CQ289849	CQ289849 Sequence
c	42	20	1.0	450	6	CQ326815	CQ326815 Sequence
	43	20	1.0	459	8	AF072341	AF072341 Ajellomyc
	44	20	1.0	459	8	AF072342	AF072342 Ajellomyc
	45	20	1.0	459	8	AF072343	AF072343 Ajellomyc

dupl

4/96 SDB Post

Dupl

1997 Photosynthesis

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 16:07:57 ; Search time 1102 Seconds  
(without alignments)  
10668.427 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1986	100.0	1986	3	AAC64431	Aac64431 Saccharom
2	1986	100.0	1986	3	AAC64440	Aac64440 Saccharom
3	1986	100.0	1986	5	AAS01342	Aas01342 Yeast LCA
4	1986	100.0	1986	12	ADF47816	Adf47816 Yeast acy

	5	1694	85.3	1701	12	ADF47817	Adf47817 Yeast mem
	6	1119	56.3	1986	3	AAC64441	Aac64441 Saccharom
	7	30	1.5	46	12	ADF47839 X	Adf47839 Yeast acy
	8	27	1.4	46	12	ADF47837 X	Adf47837 Yeast acy
	9	25	1.3	41	12	ADF47838 X	Adf47838 Yeast acy
c	10	20	1.0	450	4	AAI11005 X	Aai11005 Probe #93
c	11	20	1.0	450	4	ABA52660 X	Aba52660 Human foe
c	12	20	1.0	450	4	AAI32267 X	Aai32267 Probe #95
c	13	20	1.0	450	4	ABA42236 X	Aba42236 Human bre
c	14	20	1.0	450	4	ABA22448 X	Aba22448 Probe #91
c	15	20	1.0	450	4	AAK26373	Aak26373 Human bon
c	16	20	1.0	450	4	AAK00918	Aak00918 Human bra
c	17	20	1.0	450	4	ABS25968	Abs25968 Human liv
c	18	20	1.0	450	5	AAI00926	Aai00926 Probe #91
c	19	20	1.0	450	6	ABS00963	Abs00963 Human gen
c	20	20	1.0	575	12	ACH68028	Ach68028 Human gen
c	21	20	1.0	792	5	AAF68302	Aaf68302 Human lun
c	22	20	1.0	792	6	ABK38213	Abk38213 cDNA enco
c	23	20	1.0	792	8	ACA10542	Aca10542 Human lun
c	24	20	1.0	792	8	ABX99493	Abx99493 Lung canc
c	25	20	1.0	792	10	ADH45739	Adh45739 Human lun
c	26	20	1.0	792	12	ADE72276	Ade72276 Human lun
c	27	20	1.0	792	13	ADJ19658	Adj19658 Human lun
	28	20	1.0	3420	10	ACF68206	Acf68206 Photorhab
c	29	20	1.0	110000	10	ACF67367_09	Continuation (10 o
c	30	20	1.0	110000	10	ACF65384_3	Continuation (4 of
	31	19	1.0	39	5	AAS01346	Aas01346 Yeast LRO
	32	19	1.0	540	4	AAK88546	Aak88546 Human dig
c	33	19	1.0	840	10	ADF02110	Adf02110 Bacterial
	34	19	1.0	951	5	AAH94468	Aah94468 Human foe
c	35	19	1.0	1056	13	ADS55204	Ads55204 Bacterial
c	36	19	1.0	1071	13	ADS49690	Ads49690 Bacterial
	37	19	1.0	1326	10	ACF71073	Acf71073 Photorhab
	38	19	1.0	1672	12	ADL13358	Adl13358 Human ste
	39	19	1.0	1819	4	AAK90612	Aak90612 Human dig
c	40	19	1.0	2000	8	ADA71449	Ada71449 Rice gene
c	41	19	1.0	2000	8	ADA72450	Ada72450 Rice gene
c	42	19	1.0	2000	12	ADJ41071	Adj41071 Plant cDN
c	43	19	1.0	2878	10	ADB68594	Adb68594 Mouse mic
	44	19	1.0	3176	13	ADR07994	Adr07994 Full leng
	45	19	1.0	3188	4	AAK90614	Aak90614 Human dig



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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 20:45:36 ; Search time 355 Seconds  
(without alignments)  
9153.931 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					
No.	Score	Match	Length	DB	ID	Description	
c 1	20	1.0	792	4	US-09-702-705-220 X	Sequence 220, App	
c 2	20	1.0	792	4	US-09-736-457-220 X	Sequence 220, App	
c 3	20	1.0	792	4	US-09-614-124B-220 X	Sequence 220, App	
c 4	20	1.0	792	4	US-09-671-325-220 X	Sequence 220, App	
c 5	20	1.0	792	4	US-09-589-184-220	Sequence 220, App	
c 6	20	1.0	792	4	US-09-658-824-220	Sequence 220, App	
7	19	1.0	601	4	US-09-949-016-72828	Sequence 72828, A	
8	19	1.0	601	4	US-09-949-016-72829	Sequence 72829, A	
9	19	1.0	601	4	US-09-949-016-72830	Sequence 72830, A	
10	19	1.0	601	4	US-09-949-016-72831	Sequence 72831, A	
11	19	1.0	601	4	US-09-949-016-72832 V	Sequence 72832, A	

	12	19	1.0	601	4	US-09-949-016-72833 X	Sequence 72833, A
c	13	19	1.0	840	4	US-09-543-681A-2395 X	Sequence 2395, Ap
	14	19	1.0	1014	4	US-09-248-796A-6352/99	Sequence 635, App 6747137
c	15	19	1.0	1023	4	US-09-248-796A-2948 //	Sequence 2948, Ap //
	16	19	1.0	1672	4	US-09-976-594-1087	Sequence 1087, Ap
c	17	19	1.0	2878	4	US-09-917-963-10	Sequence 10, Appl
c	18	19	1.0	4267	3	US-09-661-753-47	Sequence 47, Appl
c	19	19	1.0	106450	4	US-09-949-016-13873	Sequence 13873, A
c	20	19	1.0	147840	4	US-09-949-016-15236	Sequence 15236, A
c	21	18	0.9	25	4	US-09-396-196G-60894	Sequence 60894, A
c	22	18	0.9	36	3	US-08-781-891-184	Sequence 184, App
c	23	18	0.9	36	4	US-09-618-166-184	Sequence 184, App
	24	18	0.9	507	4	US-09-248-796A-11763	Sequence 11763, A
	25	18	0.9	601	4	US-09-949-016-115126	Sequence 115126,
	26	18	0.9	601	4	US-09-949-016-116421	Sequence 116421,
	27	18	0.9	601	4	US-09-949-016-116422	Sequence 116422,
c	28	18	0.9	601	4	US-09-949-016-177105	Sequence 177105,
	29	18	0.9	601	4	US-09-949-016-203275	Sequence 203275,
c	30	18	0.9	1590	4	US-09-489-039A-2550	Sequence 2550, Ap
	31	18	0.9	2090	4	US-09-270-767-12599	Sequence 12599, A
	32	18	0.9	2106	4	US-09-248-796A-1147	Sequence 1147, Ap
	33	18	0.9	2148	4	US-09-543-681A-3431	Sequence 3431, Ap
c	34	18	0.9	3507	1	US-08-315-468-3	Sequence 3, Appli
c	35	18	0.9	3513	4	US-09-815-923-13	Sequence 13, Appl
c	36	18	0.9	9060	3	US-08-378-313-20	Sequence 20, Appl
c	37	18	0.9	19703	4	US-09-949-016-14926	Sequence 14926, A
	38	18	0.9	25512	4	US-09-949-016-15886	Sequence 15886, A
	39	18	0.9	25512	4	US-09-949-016-15887	Sequence 15887, A
	40	18	0.9	49472	4	US-09-949-016-17478	Sequence 17478, A
	41	18	0.9	50878	4	US-09-949-016-11787	Sequence 11787, A
	42	18	0.9	92344	4	US-09-949-016-16802	Sequence 16802, A
	43	18	0.9	93364	4	US-09-949-016-14890	Sequence 14890, A
	44	18	0.9	101349	4	US-09-949-016-17433	Sequence 17433, A
	45	18	0.9	173787	4	US-09-949-016-12542	Sequence 12542, A

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 20:51:36 ; Search time 1200 Seconds  
(without alignments)  
10075.121 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5642217 seqs, 3043843248 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	21	1.1	183334	19	US-10-741-600-17646	X	Sequence 17646, A
c 2	20	1.0	367	18	US-10-425-115-147325		Sequence 147325,
c 3	20	1.0	450	9	US-09-864-761-914		Sequence 914, App
c 4	20	1.0	575	16	US-10-029-386-1223		Sequence 1223, Ap
c 5	20	1.0	792	9	US-09-736-457-220		Sequence 220, App
c 6	20	1.0	792	9	US-09-902-941-220		Sequence 220, App
c 7	20	1.0	792	9	US-09-849-626-220		Sequence 220, App
c 8	20	1.0	792	10	US-09-476-300-220		Sequence 220, App
c 9	20	1.0	792	14	US-10-017-754-220		Sequence 220, App
c 10	20	1.0	792	16	US-10-113-872-220		Sequence 220, App
c 11	20	1.0	792	17	US-10-283-017-220		Sequence 220, App
12	20	1.0	834	18	US-10-437-963-91894		Sequence 91894, A
c 13	20	1.0	1660	17	US-10-424-599-109347		Sequence 109347,
c 14	20	1.0	3089	18	US-10-425-115-109147		Sequence 109147,
c 15	20	1.0	4833	18	US-10-425-115-177412		Sequence 177412,
16	20	1.0	4950	18	US-10-425-115-109152		Sequence 109152,
c 17	20	1.0	5433	18	US-10-425-115-177411		Sequence 177411,
c 18	19	1.0	25	19	US-10-719-900-547596		Sequence 547596,
c 19	19	1.0	201	18	US-10-719-993-17098		Sequence 17098, A
20	19	1.0	201	18	US-10-719-993-43317		Sequence 43317, A
21	19	1.0	415	18	US-10-437-963-15580		Sequence 15580, A
c 22	19	1.0	740	18	US-10-437-963-67956		Sequence 67956, A
c 23	19	1.0	1056	17	US-10-369-493-30878		Sequence 30878, A
c 24	19	1.0	1071	17	US-10-369-493-28120		Sequence 28120, A
25	19	1.0	1930	17	US-10-425-114-26751		Sequence 26751, A
c 26	19	1.0	2000	17	US-10-260-238-2071		Sequence 2071, Ap
c 27	19	1.0	2878	10	US-09-917-963-10		Sequence 10, Appl
c 28	19	1.0	2878	19	US-10-764-420-2702		Sequence 2702, Ap
29	19	1.0	3007	18	US-10-425-115-173430		Sequence 173430,
c 30	19	1.0	3192	18	US-10-425-115-87876		Sequence 87876, A
31	19	1.0	3822	18	US-10-664-705-148		Sequence 148, App
32	19	1.0	3864	17	US-10-369-493-25515		Sequence 25515, A
c 33	19	1.0	4267	10	US-09-948-002-47		Sequence 47, Appl
c 34	19	1.0	4267	17	US-10-189-267-11		Sequence 11, Appl
c 35	19	1.0	4267	17	US-10-633-163-47		Sequence 47, Appl
36	19	1.0	5218	17	US-10-310-154-250		Sequence 250, App
37	19	1.0	10006	15	US-10-311-455-9		Sequence 9, Appli
38	19	1.0	13051	18	US-10-719-993-6932		Sequence 6932, Ap
c 39	19	1.0	50287	13	US-10-087-192-1501		Sequence 1501, Ap
c 40	19	1.0	107829	13	US-10-087-192-361		Sequence 361, App
41	19	1.0	168407	18	US-10-322-281-305		Sequence 305, App
c 42	19	1.0	366803	18	US-10-719-993-6805		Sequence 6805, Ap
c 43	18	0.9	25	19	US-10-809-189-60894		Sequence 60894, A
c 44	18	0.9	36	17	US-10-374-077-184		Sequence 184, App
45	18	0.9	260	11	US-09-922-293-1957		Sequence 1957, Ap

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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 20:25:31 ; Search time 6685 Seconds  
(without alignments)  
11308.248 Million cell updates/sec

Title: US-09-937-779-1  
Perfect score: 1986  
Sequence: 1 atgggcacactgtttcgaag.....agatgcccttcccaatgtaa 1986

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
c	1	23	1.2	400	8	AZ924376	Dupl	AZ924376 4906.ic28
	2	22	1.1	553	8	AZ525082	X	AZ525082 240PbA04
c	3	22	1.1	564	6	CD847546	X	CD847546 DH0AB60ZH
c	4	22	1.1	620	7	CF077965		CF077965 QHK17N06.
c	5	22	1.1	752	5	BU026006		BU026006 QHG12L10.
	6	21	1.1	181	8	BH738251		BH738251 BOHXI49TR
	7	21	1.1	183	7	CF918634		CF918634 Bflor498.
	8	21	1.1	184	7	CF918690		CF918690 Bflor498.

	9	21	1.1	256	7	CN191467	CN191467	UCRCS06_0
c	10	21	1.1	288	4	BJ454259	BJ454259	BJ454259
c	11	21	1.1	288	9	CL206068	CL206068	ZMMBBb057
	12	21	1.1	338	8	BH440971	BH440971	BOGON75TF
c	13	21	1.1	386	4	BM443004	BM443004	EBro02_SQ
	14	21	1.1	393	8	BH690705	BH690705	BOMMI93TR
	15	21	1.1	403	8	B03865	B03865	cSRL-18h9-u
	16	21	1.1	439	4	BJ461791	BJ461791	BJ461791
	17	21	1.1	457	4	BI385211	BI385211	BFLG2_003
c	18	21	1.1	461	9	CL245339	CL245339	ZMMBBb039
	19	21	1.1	464	8	BH439796	BH439796	BOHCL92TR
	20	21	1.1	485	4	BI385212	BI385212	BFLG2_003
	21	21	1.1	537	8	BH461140	BH461140	BOHNT40TR
	22	21	1.1	554	8	BH590618	BH590618	BOGFL54TF
	23	21	1.1	573	8	AQ778682	AQ778682	HS_2235_A
c	24	21	1.1	596	8	BH669448	BH669448	BOMEZ73TF
c	25	21	1.1	597	6	CD055309	CD055309	HO08N23S
	26	21	1.1	598	9	CC948120	CC948120	BOIBR05TF
	27	21	1.1	601	8	BH650596	BH650596	BOHYC18TR
c	28	21	1.1	605	8	BH720093	BH720093	BOMLN41TR
	29	21	1.1	607	8	BH455709	BH455709	BOHSH59TF
c	30	21	1.1	622	5	BQ793370	BQ793370	EST_2308
	31	21	1.1	633	7	CK403317	CK403317	AUF_IfHdk
	32	21	1.1	639	8	BH424160	BH424160	BOGTH82TR
c	33	21	1.1	639	9	CG737180	CG737180	ZMMBBb032
	34	21	1.1	642	8	BH682774	BH682774	BOHUS05TR
c	35	21	1.1	649	5	BQ793616	BQ793616	EST_2554
c	36	21	1.1	664	9	CC968690	CC968690	BOIFI86TF
c	37	21	1.1	667	8	BH250391	BH250391	BOGAZ39TR
	38	21	1.1	668	8	BH688265	BH688265	BOHTG70TR
	39	21	1.1	680	8	BH972432	BH972432	odj04f09.
	40	21	1.1	680	8	BZ072897	BZ072897	1kg71g09.
c	41	21	1.1	688	8	AQ953709	AQ953709	Sheared D
	42	21	1.1	694	8	BZ047486	BZ047486	1ki21b09.
	43	21	1.1	695	8	BH541538	BH541538	BOGRX05TF
	44	21	1.1	696	8	BH734523	BH734523	BOMIQ76TR
	45	21	1.1	696	8	BH930691	BH930691	odj01e06.

↓  
1996 primers

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 2, 2005, 11:27:24 ; Search time 7744 Seconds  
(without alignments)  
4135.963 Million cell updates/sec

Title: US-09-937-779-2  
Perfect score: 3546  
Sequence: 1 MGTLFRRNVQNQKSDSDENN.....VEPRQLSNLSQWVSQMPFPM 661

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09937779/runat\_02052005\_122715\_18261/app\_query.fasta\_1.8  
39

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09937779@cgn\_1\_1\_4545@runat\_02052005\_122715\_18261 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	3546	100.0	1986	6	BD271616	BD271616 Novel cla	
2	3546	100.0	1986	6	BD271625	BD271625 Novel cla	
3	3546	100.0	1986	6	BD271626	BD271626 Novel cla	
4	3546	100.0	1986	6	AX037577	AX037577 Sequence	
5	3546	100.0	1986	6	AX037595	AX037595 Sequence	
6	3546	100.0	1986	6	AX037597	AX037597 Sequence	
7	3546	100.0	1986	6	AX090382	AX090382 Sequence	
8	3546	100.0	2575	8	SCYNR008W	Z71623 S.cerevisia	
9	3546	100.0	23901	8	SCN201952	X77395 S.cerevisia	
c 10	2469	69.6	110000	8	CR380955_05	Continuation (6 of	
c 11	2244.5	63.3	110000	8	AE016819_00	AE016819 Eremothec	
c 12	2244.5	63.3	110000	8	AE016819_01	Continuation (2 of	
c 13	2220.5	62.6	110000	8	CR382126_06	Continuation (7 of	
14	1840	51.9	110000	8	CR382136_07	Continuation (8 of	
15	1840	51.9	110000	8	CR382136_08	Continuation (9 of	
16	1769	49.9	2106	6	AR546016	AR546016 Sequence	
c 17	1630	46.0	110000	8	CR382131_19	Continuation (20 o	
18	1245.5	35.1	103568	8	CNS07EGJ	AL590462 DNA centr	
c 19	1245.5	35.1	322194	8	CNS09S4S	BX088700 DNA centr	
20	1150.5	32.4	2312	6	BD271617	BD271617 Novel cla	
21	1150.5	32.4	2312	6	BD271627	BD271627 Novel cla	
22	1150.5	32.4	2312	6	AX037579	AX037579 Sequence	
23	1150.5	32.4	2312	6	AX037599	AX037599 Sequence	
24	1150.5	32.4	42391	8	SPBC776	AL035263 S.pombe c	
25	852	24.0	4093	6	AX794722	AX794722 Sequence	
26	845.5	23.8	2828	8	AY210981	AY210981 Medicago	
27	839.5	23.7	2433	6	AX794708	AX794708 Sequence	
28	839.5	23.7	2495	8	AK100079	AK100079 Oryza sat	
29	839.5	23.7	2565	6	AX794706	AX794706 Sequence	
30	836.5	23.6	2479	6	AX794704	AX794704 Sequence	
31	835	23.5	2700	6	AX794710	AX794710 Sequence	
32	832.5	23.5	2441	8	BT013705	BT013705 Lycopersi	
33	832	23.5	2013	6	AX090380	AX090380 Sequence	
34	832	23.5	2016	6	AX412864	AX412864 Sequence	
35	832	23.5	2402	8	AY052715	AY052715 Arabidops	
36	832	23.5	2425	6	AX925713	AX925713 Sequence	
37	828	23.4	2398	6	AX794712	AX794712 Sequence	
38	823	23.2	2427	6	BD271619	BD271619 Novel cla	
39	823	23.2	2427	6	AX037581	AX037581 Sequence	
40	823	23.2	2431	8	AY160110	AY160110 Arabidops	
41	819	23.1	2030	6	AX794714	AX794714 Sequence	
c 42	758.5	21.4	39475	2	AC149358	AC149358 Phakopsor	
43	724	20.4	3203	8	AK099811	AK099811 Oryza sat	



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 2, 2005, 11:27:24 ; Search time 1036 Seconds  
(without alignments)  
3776.978 Million cell updates/sec

Title: US-09-937-779-2  
Perfect score: 3546  
Sequence: 1 MGTLFRRNVQNQKSDSDENN.....VEPRQLSNLSQWVSQMPFFPM 661

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09937779/runat\_02052005\_122714\_18249/app\_query.fasta\_1.8  
39

-DB=N\_Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09937779 @CGN\_1\_1\_470 @runat\_02052005\_122714\_18249 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*

11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3546	100.0	1986	3	AAC64431	Aac64431 Saccharom
2	3546	100.0	1986	3	AAC64440	Aac64440 Saccharom
3	3546	100.0	1986	5	AAS01342	Aas01342 Yeast LCA
4	3546	100.0	1986	12	ADF47816	Adf47816 Yeast acy
5	3481	98.2	1986	3	AAC64441	Aac64441 Saccharom
6	3029	85.4	1701	12	ADF47817	Adf47817 Yeast mem
7	1269	35.8	1872	12	ADF47831	Adf47831 Schizosac
c 8	1182	33.3	7299	13	ADR84383	Adr84383 Aspergill
9	1165.5	32.9	2223	12	ADF47830	Adf47830 Aspergill
10	1155	32.6	2047	12	ADF47829	Adf47829 Aspergill
11	1150.5	32.4	2312	3	AAC64432	Aac64432 Schizosac
12	1132.5	31.9	2312	3	AAC64442	Aac64442 Schizosac
13	852	24.0	4093	9	AAL62913	Aal62913 Soybean c
14	839.5	23.7	2433	9	AAL62907	Aal62907 Rice cDNA
15	839.5	23.7	2565	9	AAL62906	Aal62906 Corn cDNA
16	838.5	23.6	2004	12	ADF47835	Adf47835 Crepis pa
17	836.5	23.6	2479	9	AAL62905	Aal62905 Guayule c
18	835	23.5	2700	9	AAL62908	Aal62908 Soybean c
19	832	23.5	2013	5	AAS01341	Aas01341 Arabidops
20	832	23.5	2016	6	ADG88186	Adg88186 A. thalia
21	832	23.5	2016	12	ADF47819	Adf47819 Arabidops
22	832	23.5	2425	10	ADG25155	Adg25155 P. patens
23	828	23.4	2398	9	AAL62909	Aal62909 Sunflower
24	823	23.2	2427	3	AAC64434	Aac64434 Arabidops
25	822.5	23.2	1803	12	ADF47821	Adf47821 Arabidops
26	819	23.1	2030	9	AAL62910	Aal62910 Wheat cDN
27	807.5	22.8	1998	8	ABZ76360	Abz76360 A. thalia
28	807.5	22.8	1998	12	ADF47827	Adf47827 Arabidops
29	806.5	22.7	2016	12	ADF47833	Adf47833 Crepis pa
30	539	15.2	3107	5	AAS01085	Aas01085 Arabidops
31	532	15.0	3685	3	AAC64433	Aac64433 Arabidops
32	526	14.8	3685	3	AAC64443	Aac64443 Arabidops
33	457.5	12.9	553	8	ABZ54921	Abz54921 Aspergill
34	410	11.6	578	13	ADR61378	Adr61378 Cotton cD
35	403	11.4	1510	9	AAL62904	Aal62904 Guar cDNA
c 36	320	9.0	1680	5	AAS01086	Aas01086 Arabidops
37	309	8.7	616	3	AAC64436	Aac64436 Neurospor
38	301.5	8.5	1902	12	ADF47823	Adf47823 Arabidops
39	299.5	8.4	1641	5	AAS01082	Aas01082 Arabidops
40	254.5	7.2	1323	6	ABK87900	Abk87900 cDNA enco
41	254.5	7.2	1358	1	AAN70191	Aan70191 DNA clone
42	254.5	7.2	1744	2	AAZ32180	Aaz32180 Human lec
43	254.5	7.2	1744	5	AAD02648	Aad02648 Human lec
44	254.5	7.2	1744	6	ABK35510	Abk35510 Human end

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 2, 2005, 11:27:24 ; Search time 306 Seconds  
(without alignments)  
3534.572 Million cell updates/sec

Title: US-09-937-779-2  
Perfect score: 3546  
Sequence: 1 MGTLFRRNVQNQKSDSDENN.....VEPRQLSNLSQWVSQMPFPM 661

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09937779/runat\_02052005\_122715\_18282/app\_query.fasta\_1.8  
39

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09937779\_@CGN\_1\_1\_69\_@runat\_02052005\_122715\_18282 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
1	1769	49.9	2106	4	US-09-248-796A-1147	Sequence 1147, Ap
2	254.5	7.2	1354	4	US-09-949-016-3703	Sequence 3703, Ap
3	254.5	7.2	1744	4	US-09-054-272-33	Sequence 33, Appl
4	254.5	7.2	1744	4	US-09-919-497-30	Sequence 30, Appl
5	246.5	7.0	1236	4	US-09-402-532-17	Sequence 17, Appl
6	245.5	6.9	1332	4	US-09-402-532-18	Sequence 18, Appl
7	244.5	6.9	1137	4	US-09-402-532-12	Sequence 12, Appl
8	244.5	6.9	1146	4	US-09-402-532-15	Sequence 15, Appl
9	243.5	6.9	1233	4	US-09-402-532-13	Sequence 13, Appl
10	243.5	6.9	1242	4	US-09-402-532-16	Sequence 16, Appl
11	242.5	6.8	1236	4	US-09-402-532-19	Sequence 19, Appl
12	237.5	6.7	1137	4	US-09-402-532-14	Sequence 14, Appl
13	233.5	6.6	2687	4	US-09-489-847-57	Sequence 57, Appl
c 14	127	3.6	2640	4	US-09-252-991A-11547	Sequence 11547, A
15	126	3.6	2934	4	US-09-252-991A-11690	Sequence 11690, A
16	123	3.5	8230	4	US-09-949-016-15445	Sequence 15445, A
17	122	3.4	552	4	US-09-248-796A-10377	Sequence 10377, A
c 18	122	3.4	2307	4	US-09-252-991A-6437	Sequence 6437, Ap
19	120	3.4	7430	4	US-08-956-171E-260	Sequence 260, App
20	120	3.4	7430	4	US-08-781-986A-260	Sequence 260, App
21	115.5	3.3	2289	4	US-09-107-532A-621	Sequence 621, App
22	114.5	3.2	2032	4	US-09-949-016-2678	Sequence 2678, Ap
23	114.5	3.2	2032	4	US-09-949-016-2700	Sequence 2700, Ap
24	114.5	3.2	6032	4	US-09-949-016-14420	Sequence 14420, A
25	114.5	3.2	6033	4	US-09-949-016-14442	Sequence 14442, A
26	113.5	3.2	1098	4	US-09-248-796A-6883	Sequence 6883, Ap
27	111	3.1	2226	4	US-09-252-991A-14877	Sequence 14877, A
c 28	111	3.1	2268	4	US-09-252-991A-14487	Sequence 14487, A
29	110.5	3.1	2038	4	US-09-949-016-1379	Sequence 1379, Ap
30	110	3.1	3114	4	US-09-543-681A-3505	Sequence 3505, Ap
c 31	109.5	3.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 32	109.5	3.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
33	107	3.0	4404	4	US-09-134-000C-3335	Sequence 3335, Ap
34	105	3.0	1380	4	US-09-252-991A-6030	Sequence 6030, Ap
35	105	3.0	1530	4	US-09-252-991A-6116	Sequence 6116, Ap
36	105	3.0	1611	4	US-09-600-099-2	Sequence 2, Appli
37	105	3.0	6436	4	US-09-600-099-1	Sequence 1, Appli
c 38	104.5	2.9	10411	3	US-08-961-527-89	Sequence 89, Appl
39	104.5	2.9	129908	4	US-09-585-858-1	Sequence 1, Appli
40	104.5	2.9	129908	4	US-10-270-878-1	Sequence 1, Appli
c 41	103	2.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 42	103	2.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
43	102.5	2.9	2169	3	US-08-806-326-5	Sequence 5, Appli
c 44	102	2.9	22807	4	US-09-902-540-1214	Sequence 1214, Ap
45	101	2.8	1077	3	US-09-155-920-1	Sequence 1, Appli

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 2, 2005, 11:27:24 ; Search time 997 Seconds  
(without alignments)  
4036.069 Million cell updates/sec

Title: US-09-937-779-2  
Perfect score: 3546  
Sequence: 1 MGTLFRRNVQNQKSDSDENN.....VEPRQLSNLSQWVSQMPFPM 661

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09937779/runat\_02052005\_122715\_18296/app\_query.fasta\_1.8  
39

-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09937779 @CGN\_1\_1\_480 @runat\_02052005\_122715\_18296  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1630	46.0	2326	19	US-10-883-760-45	Dup/	Sequence 45, Appl
2	852	24.0	4093	17	US-10-321-802-35	X	Sequence 35, Appl
3	839.5	23.7	2433	17	US-10-321-802-21		Sequence 21, Appl
4	839.5	23.7	2565	17	US-10-321-802-19		Sequence 19, Appl
5	836.5	23.6	2479	17	US-10-321-802-17		Sequence 17, Appl
c 6	835	23.5	2395	18	US-10-437-963-38278		Sequence 38278, A
7	835	23.5	2700	17	US-10-321-802-23		Sequence 23, Appl
8	828	23.4	2398	17	US-10-321-802-25		Sequence 25, Appl
9	824.5	23.3	2700	18	US-10-425-115-55049		Sequence 55049, A
10	819	23.1	2030	17	US-10-321-802-27		Sequence 27, Appl
11	814	23.0	2838	17	US-10-424-599-125713		Sequence 125713,
12	807.5	22.8	1998	16	US-10-217-939-5		Sequence 5, Appli
c 13	576.5	16.3	1388	18	US-10-425-115-55048		Sequence 55048, A
14	410	11.6	578	18	US-10-767-795-2159		Sequence 2159, Ap
15	403	11.4	1510	17	US-10-321-802-15		Sequence 15, Appl
16	357.5	10.1	735	18	US-10-437-963-38267		Sequence 38267, A
17	298	8.4	1141	17	US-10-424-599-124418		Sequence 124418,
18	293	8.3	887	18	US-10-767-701-9911		Sequence 9911, Ap
19	254.5	7.2	1744	9	US-09-919-497-30		Sequence 30, Appl
20	254.5	7.2	1744	9	US-09-880-107-2245		Sequence 2245, Ap
21	246.5	7.0	1236	16	US-10-323-051-17		Sequence 17, Appl
22	246.5	7.0	1400	18	US-10-755-889-577		Sequence 577, App
23	246.5	7.0	2680	9	US-09-978-295A-156		Sequence 156, App
24	246.5	7.0	2680	9	US-09-978-697-156		Sequence 156, App
25	246.5	7.0	2680	9	US-09-978-192A-156		Sequence 156, App
26	246.5	7.0	2680	9	US-09-999-832A-156		Sequence 156, App
27	246.5	7.0	2680	10	US-09-978-189-156		Sequence 156, App
28	246.5	7.0	2680	10	US-09-978-608A-156		Sequence 156, App
29	246.5	7.0	2680	10	US-09-978-585A-156		Sequence 156, App
30	246.5	7.0	2680	10	US-09-978-191A-156		Sequence 156, App
31	246.5	7.0	2680	10	US-09-978-403A-156		Sequence 156, App
32	246.5	7.0	2680	10	US-09-978-564A-156		Sequence 156, App
33	246.5	7.0	2680	10	US-09-999-833A-156		Sequence 156, App
34	246.5	7.0	2680	10	US-09-981-915A-156		Sequence 156, App
35	246.5	7.0	2680	10	US-09-978-824-156		Sequence 156, App

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 2, 2005, 11:27:24 ; Search time 5595 Seconds  
(without alignments)  
4496.958 Million cell updates/sec

Title: US-09-937-779-2  
Perfect score: 3546  
Sequence: 1 MGLFRNRNVQNKSDSDENN.....VEPRQLSNLSQWVSQMPFPM 661

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09937779/runat\_02052005\_122715\_18269/app\_query.fasta\_1.8  
39

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000  
-USER=US09937779\_@CGN\_1\_1\_3437\_@runat\_02052005\_122715\_18269 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	1274	35.9	948	9	CNS06Y94	AL420734 T3 end of
	2	1188.5	33.5	832	9	CNS060AQ	AL407832 T7 end of
	3	1020	28.8	978	9	CNS06TH7	AL414545 T7 end of
	4	964	27.2	609	8	BZ297416	BZ297416 CG3420.fl
	5	805	22.7	783	7	CO026714	CO026714 EST805098
c	6	804.5	22.7	882	9	CNS07EA9	AL441511 T7 end of
	7	732	20.6	899	7	CO003381	CO003381 EST791716
c	8	687	19.4	474	8	AZ928292	AZ928292 479.dif06
c	9	685	19.3	400	8	AZ924376	AZ924376 4906.ic28
c	10	658.5	18.6	509	8	BZ302540	BZ302540 KD1890.q1
	11	636	17.9	1490	6	CA731511	CA731511 wiplc.pk0
c	12	632	17.8	849	9	CNS06V5M	AL416720 T7 end of
	13	599.5	16.9	970	7	CO032392	CO032392 EST810776
	14	586	16.5	512	8	BZ301369	BZ301369 KD1229.q1
	15	544.5	15.4	844	6	CB631429	CB631429 OSIEb08P
c	16	525.5	14.8	550	7	CF884811	CF884811 tric042xm
	17	513	14.5	854	4	BG645669	BG645669 EST507288
	18	486	13.7	821	4	BM780050	BM780050 EST590626
	19	482.5	13.6	724	5	BQ803421	BQ803421 WHE2837_D
c	20	475.5	13.4	972	7	CF704243	CF704243 CCAC369TO
	21	474.5	13.4	719	5	BQ865802	BQ865802 QGC5021.y
c	22	452	12.7	885	7	CF820303	CF820303 EST697685
	23	450.5	12.7	867	7	CF821111	CF821111 EST698493
	24	448	12.6	1005	6	CD458189	CD458189 Fg08_10b0
c	25	446	12.6	943	7	CF821110	CF821110 EST698492
	26	443.5	12.5	834	7	CF820302	CF820302 EST697684
c	27	442	12.5	941	7	CO032391	CO032391 EST810775
	28	433.5	12.2	674	4	BJ480170	BJ480170 BJ480170
	29	429.5	12.1	634	5	BQ870476	BQ870476 QGD9C14.y
	30	426.5	12.0	628	4	BJ478864	BJ478864 BJ478864
	31	425	12.0	874	4	BI951204	BI951204 HVSME1002
c	32	417	11.8	884	7	CO003380	CO003380 EST791715
	33	416.5	11.7	595	7	CO135652	CO135652 EST830323
c	34	416	11.7	847	7	CF685131	CF685131 CCAGP17TF
	35	416	11.7	902	7	CF704247	CF704247 CCAC369TR
c	36	414.5	11.7	835	7	CF705715	CF705715 CCABG95TF
c	37	414.5	11.7	836	7	CF697237	CF697237 CCAB181TF
c	38	414.5	11.7	858	7	CF705450	CF705450 CCAAF15TF
	39	412.5	11.6	575	1	AV938810	AV938810 AV938810
	40	408.5	11.5	610	4	BJ472152	BJ472152 BJ472152
c	41	408.5	11.5	715	7	CF706790	CF706790 CCAHD40TF
	42	406.5	11.5	596	7	CN846346	CN846346 PG07016B0
	43	401.5	11.3	731	1	AJ639263	AJ639263 AJ639263
	44	398	11.2	727	6	CD825529	CD825529 BN25.061A
	45	397.5	11.2	605	2	BE450991	BE450991 EST401878